**Seeley Lab rsfMRI preprocessing instructions**
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<u>**Directory Setup:**</u>
Each subject has a top-level directory which is typically named with subjectID
and date but not a requirement. The script only looks for folder structure and files
within the top-level directory.

To setup a subject, create the following structure:
**<top_level_directory>/:**
    **struc/**:
        **strucraw/:** Put only the raw 3D .nii structural T1 file in struc/strucraw/
    **rsfmri/:**
        **rawfmri/:** Put only the raw 3D .nii BOLD fMRI files in rsfmri/rawfmri/

<u>**To run:**</u>

**Prior to launching the Toolbox:**

- In Matlab, create a cell array variable that lists **<top_level_directory>/rsfmri/**

for all of your subjects, like so:

subjdir={' /data5/patientNIC/10886/10886_20110621/rsfmri'

'/data5/patientNIC/10886/10886_20120109/rsfmri'

'/data5/patientNIC/12162/12162_20110509/rsfmri'};

- Save the variable into a .mat file:

save('subjdir_3_subjects.mat','subjdir')

-Add the SeeleyPreprocess directory to your Matlab path

**Launching the Toolbox and running your jobs:**

-Launch the Seeley Preprocessing Toolbox by running the command:
'Preprocess' in the matlab terminal.

-When prompted select the .mat file with your subjdir variable.

-CHECK PARAMETERS: Review default parameters listed under "Pipeline
Specifications" if your basic parameters differ or you would like to run a different
configuration, click on "View & Edit Default Parameters"

It is important to check the basic parameters and customize them for your
scanner/protocol characteristics. These include TR, Number of TRs and Slice

Order. If you used an ascending or descending acquisition for your rsfMRI images, make sure you disable "Interleave Correct" under the 'Advanced Scanner Parameters' section.

-SCAN DIRECTORIES: When the "Pipeline Specifications" panel displays your desired configuration hit the "Scan Subject Directories" button. This will go into each of your subject's directories and will determine if the correct number of functional and structural files exist, corresponding to the user defined number of TRs and rsfMRI/Structural image prefixes.

After scanning completes, if the number listed under "Subjects ready to preprocess" does not match your number of subjects, check the failed subject listings by clicking the buttons next to each fail category and check the listed subject's directories to make sure they have the correct number of scans and the correct file prefixes.

-RUN: When the "Subjects ready to preprocess" count matches the count of your subject list, the last step before hitting run is to specify the processing type:

> Parallel Processing- requires Sun Grid Engine to be installed, configured and "qsub" must be on the path. Matlab will pass to whatever queues are available to qsub. Each subject will be run on its own display-free instance of matlab in the background. Logs are saved to the subjects log directory in interfmri_<output suffix> as text files that begin with e (errors) and o (stdout).

> Serial Processing- Runs all subjects within the current matlab session, one at a time. If a subject in the list fails, the next subject will begin processing and an error log will be saved to the failed subject's interfmri_<output suffix>/log directory named PreprocError.mat

Hit Run and refer to the command window in matlab for progress on job submission to SGE (if parallel) or progress on running each subject (if serial).

-CHECKING PROCESSING COMPLETION: See the Post-Processing Directory Organization Chart on the next page. A subject that completes successfully will have output images in the **processedfmri_<analysis_suffix>/images/** folder. These images are used as input to the first level analyses.

**Post-Processing Directory Organization:**
Each subject's data will be organized in the following fashion after preprocessing:
**<top_level_directory>/:**
 **struc/:**
        strucraw/: contains raw structural T1 .nii file
        strucprocessed_<analysis_suffix>: contains processed T1 .nii files
                                including skull stripped image (_brain) used for
                                coregistration

**rsfmri/:**
        **rawfmri/:** contains all raw 3D .nii BOLD fMRI files
        *\**interfmri_<analysis_suffix>/:** where all intermediate files between
                                raw and processed data are
                *\**images/:** contains all 3D .nii fMRI files from intermediate
                        stages of preprocessing
                *\**melodic.ica/:** melodic ICA directory
                motion_corr: motion correction file directory
                motion_report.png: image file used to check fMRI
                                motion. Main values to check are "Max trans"
                                (< 3 mm), "max rot" (< 3 degrees), "# spikes"
                                (~ < 10% of total number of volumes)
                *\**log/:** stores SPM job files and the subject-tailored
                        rsfmri_preprocess_MASTER.m script
                        example_func2standard.png: image file used to check
                        fMRI normalization quality
                *\**processedfmri_<analysis_suffix>/:**
                        *\**images/:** contains all 3D .nii fMRI files after all
                                preprocessing is done
**\*Folders created by Preprocessing**

**A bit of detail:**
RunSGEpreproc_MASTER calls a script named
/data/mridata/truji/SGE_PreProc/PrepPreprocCloud.m
PrepPreprocCloud.m automatically finds the paths/filenames for all of the fMRI
and structural files and stores them in a variable called preprocSetup.mat
RunSGEpreproc_MASTER updates a template of the main preprocessing script
(rsfmri_preprocess_MASTER.m) that is customized for the current subject
RunSGEpreproc_MASTER  then calls a script qsub_run_MASTER that submits
the subject-tailored rsfmri_preprocess_MASTER.m file to the cluster